

Cutaneous Lesions

Cutaneous lymphoid lesions are frequently encountered in skin biopsies. **Differentiating between various benign and malignant entities** is critical, as is a precise classification of cutaneous lymphoid infiltrate remains a vexing problem for clinicians and pathologists.

Genomic Testing Cooperative's comprehensive testing can resolve this clinical and diagnostic problem.

GTC's Hematology Profile Plus Provides

Comprehensive and **sensitive profile of mutations** distinguishing between benign and malignant process

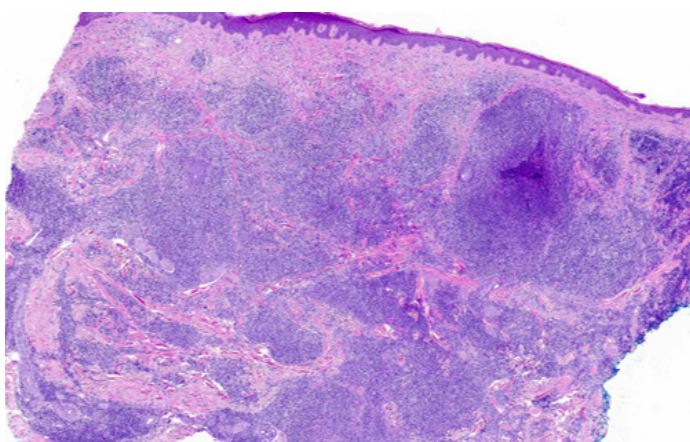
Comprehensive clonality evaluation of **B- and T-cell clonality** including heavy and light chains for B-cells, alpha, beta, gamma, and delta T-cell receptors with defining the expressed gene family so multiple lesions can be compared

Complete **immunophenotyping** profiling of the lymphoid cells (CD19, CD20, CD22, CD3, CD4, CD8, CD5, CD7, CD30, ...)

Detection of **EBV, HPV, and HTLV1** viruses

Complete chromosomal gain or loss and translocations

Detect **CAR-T T-cell lymphomas**



Don't accept partial results!

Order Hematology Profile Plus on skin biopsies and resolve the diagnostic dilemma of cutaneous lymphoid lesions.

Send samples via FFPE block or unstained slides (6 to 8 plus H&E) and follow the instructions on our website.

Cutaneous Lesions

NGS in **Melanocytic Lesions** and **Skin Sarcomas**

GTC's Solid Tumor Profile Plus Provides

Parallel DNA & RNA sequencing detects mutations, copy number changes and fusions

RNA expression profiling quantifies **oncogene/tumor suppressor activity** and **immune markers**

Provides tumor mutational burden (**TMB**), Microsatellite instability (**MSI**), UV signatures, actionable variants

Melanocytic Lesions: Benign vs Malignant Profiles

Benign nevi: **isolated driver mutation** (BRAF, NRAS) with low proliferative/**immune expression signatures**

Melanomas: accumulate progression mutations (TERT, TP53, NF1)

RNA expressions can **classify ambiguous lesions**

Skin Sarcomas

Dermatofibrosarcoma Protuberans: COL1A1-PDGFB fusion drives **PDGFB overexpression** detectable on RNAseq; predicts imatinib response

Angiosarcoma: Overexpression of angiogenesis genes (VEGFA, KDR, FLT1) + RNA-based immune signatures predict benefit from anti-VEGF agents and immunotherapy

Epithelioid Sarcoma: **SMARCB1 loss** produces characteristic **EZH2-driven transcriptional repression**; RNA profiling shows silencing of tumor suppressors, rationale for tazemetostat therapy

